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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/755,325

DATE: 03/15/2001  
 TIME: 16:26:51

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ENTERED

5 <110> APPLICANT: Hemmati-Brivanlou, Ali  
 7 Weinstein, Daniel C.  
 11 <120> TITLE OF INVENTION: TRANSLATION INITIATION FACTOR 4AIII, AND METHODS OF USE  
 13 THEREOF  
 17 <130> FILE REFERENCE: 600-1-211 N  
 21 <140> CURRENT APPLICATION NUMBER: 09/755,325  
 23 <141> CURRENT FILING DATE: 2001-01-05  
 25 <150> PRIOR APPLICATION NUMBER: 09/318,443  
 26 <151> PRIOR FILING DATE: 1999-05-25  
 31 <160> NUMBER OF SEQ ID NOS: 12  
 35 <170> SOFTWARE: PatentIn Ver. 2.0  
 39 <210> SEQ ID NO: 1  
 41 <211> LENGTH: 1245  
 43 <212> TYPE: DNA  
 45 <213> ORGANISM: Xenopus laevis  
 49 <400> SEQUENCE: 1  
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 53 ttacgggagg aggatatgac caccgtggag ttccagacca gcgaagaagt ggatgtaacg 120  
 55 ccaacgtttg atacgatggg gctgagggaa gaccttctga gaggcatacta tgcttatgga 180  
 57 ttgagaaac catcggctat acaacagaag gcaatcaagc agatcatcaa aggaagggat 240  
 59 gtgatcgac aatcacagtc tggtagcaggc aaaacagcaa ctttttgtgt ttctgtgcta 300  
 61 cagtgtttgg atattcagat cagtgaacc caagccttga ttttagcacc caccaaagag 360  
 63 tttagcacgc aaattcagaa ggtgttgctt gctttggggg actacatgaa tgtgcagtgt 420  
 65 catgcgtgta ttggaggcac aaatgttgga gaggatatcc gaaaattgga ttatgggcag 480  
 67 cagcttgttg ctggaacacc agggcgtgtt tttgatatga ttcgacgcag aagtttaaga 540  
 69 actcgggcca ttaaaatgtt agtgctggat gaagctgatg aaatgttgaa taagggtttc 600  
 71 aaggagcaaa tttatgatgt atacaggtat ctgcctccag caacacaagt ttgtttaatc 660  
 73 agtgctaccc tgccacatga aatcctggaa atgaccaata agtttatgac tgatcccatc 720  
 75 cgtatccttg tgaacgtga tgagttgaca ctggaaggca tcaagcagtt tttgtggca 780  
 77 gtggagagag aagagtggaa atttgatact ttgtgtgatt tatatgacac ttgtactatt 840  
 79 acacaagctg taatcttctg caacacaaaa agaaaggtag attggttgac tgaaaaaatg 900  
 81 agagaagcaa atttcacagt ttcgtcaatg catggtgata tgccccaaaa ggagagagag 960  
 83 tcaatcatga aagaattccg atctggtgca agccgagtc tcatatcaac ggacgtctgg 1020  
 85 gcccgaggat tggatgtgcc acaggtctcc ttgattatca actatgatct tcccaataac 1080  
 87 cgagaattgt acattcacag aattggccga tcaggaagat atggaagaaa ggtgttgcc 1140  
 89 attaaccttg tcaagaatga tgacatccgt attttaagag atattgagca gtactattcg 1200  
 91 acccagattg atgaaatgcc aatgaacggt gctgatctta ttgga 1245  
 95 <210> SEQ ID NO: 2  
 97 <211> LENGTH: 415  
 99 <212> TYPE: PRT  
 101 <213> ORGANISM: Xenopus laevis  
 105 <400> SEQUENCE: 2  
 107 Met Ala Ala Ala Val Ala Gly Val Ala Gly Leu Thr Thr Ala His  
 109 1 5 10 15  
 113 Ala Lys Arg Leu Leu Arg Glu Glu Asp Met Thr Thr Val Glu Phe Gln  
 115 20 25 30  
 119 Thr Ser Glu Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu

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121          35          40          45
125 Arg Glu Asp Leu Leu Arg Gly Ile Tyr Ala Tyr Gly Phe Glu Lys Pro
127          50          55          60
131 Ser Ala Ile Gln Gln Lys Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp
133 65          70          75          80
137 Val Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Cys
139          85          90          95
143 Val Ser Val Leu Gln Cys Leu Asp Ile Gln Ile Arg Glu Thr Gln Ala
145          100          105          110
149 Leu Ile Leu Ala Pro Thr Lys Glu Leu Ala Arg Gln Ile Gln Lys Val
151          115          120          125
155 Leu Leu Ala Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile
157          130          135          140
161 Gly Gly Thr Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln
163 145          150          155          160
167 His Val Val Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg
169          165          170          175
173 Arg Ser Leu Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala
175          180          185          190
179 Asp Glu Met Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr
181          195          200          205
185 Arg Tyr Leu Pro Pro Ala Thr Gln Val Cys Leu Ile Ser Ala Thr Leu
187          210          215          220
191 Pro His Glu Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile
193 225          230          235          240
197 Arg Ile Leu Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln
199          245          250          255
203 Phe Phe Val Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys
205          260          265          270
209 Asp Leu Tyr Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn
211          275          280          285
215 Thr Lys Arg Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn
217          290          295          300
221 Phe Thr Val Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu
223 305          310          315          320
227 Ser Ile Met Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser
229          325          330          335
233 Thr Asp Val Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile
235          340          345          350
239 Ile Asn Tyr Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile
241          355          360          365
245 Gly Arg Ser Gly Arg Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val
247          370          375          380
251 Lys Asn Asp Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser
253 385          390          395          400
257 Thr Gln Ile Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile Glx
259          405          410          415
265 <210> SEQ ID NO: 3
267 <211> LENGTH: 532

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271 <213> ORGANISM: Homo sapiens
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279 gccaccttca gtatctcagt cctccagtgt ttggatattc aggttcgtga aactcaagct 120
281 ttgatcttgg ctcccacaag agagttggct gtgcagatcc agaaggggct gcttgctctc 180
283 ggtgactaca tgaatgtcca gtgccatgcc tgcattggag gcaccaatgt tggcgaggac 240
285 atcaggaagc tggattacgg acagcatggt gttgcgggca ctccagggcg tgtttttgat 300
287 atgattcgtc gcagaagcct aaggacacgt gctatcaaaa tgttggtttt ggatgaagct 360
289 gatgaaatgt tgaataaagg tttcaaagag cagatttacg atgtatacag gtacctgcct 420
291 ccagccacac aggtggttct catcagtgcc acgctgccac acgagattct ggagatgacc 480
293 aacaagttca tgaccgaccc aatccgcac ttggtgggaa ttctgcagc cc 532
297 <210> SEQ ID NO: 4
299 <211> LENGTH: 177
301 <212> TYPE: PRT
303 <213> ORGANISM: Homo sapiens
307 <400> SEQUENCE: 4
309 Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala Gln Ser Gln Ser Gly
311 1 5 10 15
315 Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val Leu Gln Cys Leu Asp
317 20 25 30
321 Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu Ala Pro Thr Arg Glu
323 35 40 45
327 Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala Leu Gly Asp Tyr Met
329 50 55 60
333 Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr Asn Val Gly Glu Asp
335 65 70 75 80
339 Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val Ala Gly Thr Pro Gly
341 85 90 95
345 Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu Arg Thr Arg Ala Ile
347 100 105 110
351 Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met Leu Asn Lys Gly Phe
353 115 120 125
357 Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu Pro Pro Ala Thr Gln
359 130 135 140
363 Val Val Leu Ile Ser Ala Thr Leu Pro His Glu Ile Leu Glu Met Thr
365 145 150 155 160
369 Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu Val Gly Ile Pro Ala
371 165 170 175
375 Ala
383 <210> SEQ ID NO: 5
385 <211> LENGTH: 1536
387 <212> TYPE: DNA
389 <213> ORGANISM: Homo sapiens
393 <400> SEQUENCE: 5
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397 cggactctga atcatggcga ccacggccac gatggcgacc tcgggctcgg cgcgaaagcg 120
399 gctgctcaaa gaggaagaca tgactaaagt ggaattcgag accagcgagg aggtggatgt 180
401 gacccccacg ttcgacacca tgggcctgcg ggaggacctg ctgcggggca tctacgctta 240

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403 cgggttttgaa aaaccatcag caatccagca acgagcaatc aagcagatca tcaaagggag 300
405 agatgtcatc gcacagtctc agtccggcac aggaaaaaca gccaccttca gtatctcagt 360
407 cctccagtgt ttggatatcc aggttcgtga aactcaagct ttgatcttgg ctcccacaag 420
409 agagttggct gtgcagatcc agaaggggct gcttgctctc ggtgactaca tgaatgtcca 480
411 gtgccatgcc tgcattggag gcaccaatgt tggcgaggac atcaggaagc tggattacgg 540
413 acagcatggt gtgcggggca ctccagggag tgtttttgat atgattcgtc gcagaagcct 600
415 aaggacacgt gctatcaaaa tgttggtttt ggatgaagct gatgaaatgt tgaataaagg 660
417 tttcaaagag cagatttacg atgtatacag gtacctgcct tcagccacac aggtggttct 720
419 catcagtgcc acgctgccac acgagattct ggagatgacc aacaagttca tgaccgaccc 780
421 aatccgcacg ttggtgaaac gtgatgaatt gactctggaa ggcacaaagc aatttttcgt 840
423 ggcagtggag agggaaagagt ggaaatttga cactctgtgt gacctctacg acacactgac 900
425 catcactcag gcggtcatct tctgcaacac caaaagaaaag gtggactggc tgacggagaa 960
427 aatgagggaa gccaaactca ctgtatcctc aatgcatgga gacatgcccc agaaagagcg 1020
429 ggagtcacat atgaaggagt tccggtcggg cgccagccga gtgcttattt ctacagatgt 1080
431 ctgggccagg gggttggatg tccctcaggt gtccctcatc attaactatg atctccctaa 1140
433 taacagagaa ttgtacatac acagaattgg gagatcaggt caatacggcc ggaaggggtg 1200
435 ggccattaac tttgtaaaga atgacgacat ccgcacctc agagatatcg agcagtacta 1260
437 ttccactcag attgatgaga tgccgatgaa cgttgctgat cttatctgaa gcagcagatc 1320
439 agtgggatga gggagactgt tcacctgctg tgtactcctg tttggaagta tttagatcca 1380
441 gattctactt aatgggggtt atattggactt tcttctcata aatggcctgc cgtctccctt 1440
443 cctttgaaga ggatatggg attctgctct cttttcttat ttacatgtaa ataatacatt 1500
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449 &lt;210&gt; SEQ ID NO: 6

451 &lt;211&gt; LENGTH: 411

453 &lt;212&gt; TYPE: PRT

455 &lt;213&gt; ORGANISM: Homo sapiens

459 &lt;400&gt; SEQUENCE: 6

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463 1 5 10 15
467 Leu Leu Lys Glu Glu Asp Met Thr Lys Val Glu Phe Glu Thr Ser Glu
469 20 25 30
473 Glu Val Asp Val Thr Pro Thr Phe Asp Thr Met Gly Leu Arg Glu Asp
475 35 40 45
479 Leu Leu Arg Gly Ile Tyr Ala Thr Gly Phe Glu Lys Pro Ser Ala Ile
481 50 55 60
485 Gln Gln Arg Ala Ile Lys Gln Ile Ile Lys Gly Arg Asp Val Ile Ala
487 65 70 75 80
491 Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Thr Phe Ser Ile Ser Val
493 85 90 95
497 Leu Gln Cys Leu Asp Ile Gln Val Arg Glu Thr Gln Ala Leu Ile Leu
499 100 105 110
503 Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Gln Lys Gly Leu Leu Ala
505 115 120 125
509 Leu Gly Asp Tyr Met Asn Val Gln Cys His Ala Cys Ile Gly Gly Thr
511 130 135 140
515 Asn Val Gly Glu Asp Ile Arg Lys Leu Asp Tyr Gly Gln His Val Val
517 145 150 155 160
521 Ala Gly Thr Pro Gly Arg Val Phe Asp Met Ile Arg Arg Arg Ser Leu
523 165 170 175

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527 Arg Thr Arg Ala Ile Lys Met Leu Val Leu Asp Glu Ala Asp Glu Met
529      180      185      190
533 Leu Asn Lys Gly Phe Lys Glu Gln Ile Tyr Asp Val Tyr Arg Tyr Leu
535      195      200      205
539 Pro Ser Ala Thr Gln Val Val Leu Ile Ser Ala Thr Leu Pro His Glu
541      210      215      220
545 Ile Leu Glu Met Thr Asn Lys Phe Met Thr Asp Pro Ile Arg Ile Leu
547 225      230      235      240
551 Val Lys Arg Asp Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Phe Val
553      245      250      255
557 Ala Val Glu Arg Glu Glu Trp Lys Phe Asp Thr Leu Cys Asp Leu Tyr
559      260      265      270
563 Asp Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Cys Asn Thr Lys Arg
565      275      280      285
569 Lys Val Asp Trp Leu Thr Glu Lys Met Arg Glu Ala Asn Phe Thr Val
571      290      295      300
575 Ser Ser Met His Gly Asp Met Pro Gln Lys Glu Arg Glu Ser Ile Met
577 305      310      315      320
581 Lys Glu Phe Arg Ser Gly Ala Ser Arg Val Leu Ile Ser Thr Asp Val
583      325      330      335
587 Trp Ala Arg Gly Leu Asp Val Pro Gln Val Ser Leu Ile Ile Asn Tyr
589      340      345      350
593 Asp Leu Pro Asn Asn Arg Glu Leu Tyr Ile His Arg Ile Gly Arg Ser
595      355      360      365
599 Gly Gln Tyr Gly Arg Lys Gly Val Ala Ile Asn Phe Val Lys Asn Asp
601      370      375      380
605 Asp Ile Arg Ile Leu Arg Asp Ile Glu Gln Tyr Tyr Ser Thr Gln Ile
607 385      390      395      400
611 Asp Glu Met Pro Met Asn Val Ala Asp Leu Ile
613      405      410
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623 <212> TYPE: DNA
625 <213> ORGANISM: Homo sapiens
629 <400> SEQUENCE: 7
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633 cagcggcaca gcgaggtcgg cagcggcaca gcgaggtcgg cagcggcaca gcgaggtcgg 120
635 cagcggcagc gaggtcggca gcggcacagc gaggtcggca gcggcagcga ggtcggcagc 180
637 ggcgcgcgct gtgctcttcc gcggactctg aatcatggcg accacggcca cgatggcgac 240
639 ctcgggctcg gcgcgaaagc ggctgctcaa agaggaagac atgactaaag tggaaattcga 300
641 gaccagcgag gaggtggatg tgaccccccac gttcgacacc atgggcctgc gggaggacct 360
643 gctgcggggc atctacgctt acggttttga aaaaccatca gcaatccagc aacgagcaat 420
645 caagcagatc atcaaaggga gagatgtcat cgcacagtct cagtccggca caggaaaaaac 480
647 agccaccttc agtatctcag tcctccagtg tttggatatt caggttcgtg aaactcaagc 540
649 tttgatcttg gtcgccacaa gagagtggc tgtgcagatc cagaaggggc tgcttgctct 600
651 cggtgactac atgaatgtcc agtgccatgc ctgcattgga ggcaccaatg ttggcgagga 660
653 catcaggaag ctggattacg gacagcatgt tgtcgcgggc actccagggc gtgtttttga 720
655 tatgattcgt cgcagaagcc taaggacaag tgctatcaaa atgttggttt tggatgaagc 780
657 tgatgaaatg ttgaataaag gtttcaaaga gcagatttac gatgtataca ggtacctgcc 840

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